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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FLECKENSTEIN, Bernhard
ENSSER, Armin
- (ii) TITLE OF INVENTION: HUMAN SEMAPHORIN L (H-SEMAL) AND
CORRESPONDING SEMAPHORINS IN OTHER SPECIES
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Frommer Lawrence & Haug LLP
 - (B) STREET: 745 Fifth Avenue
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10151
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US NYA
 - (B) FILING DATE: 09-JUL-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lawrence, William F.
 - (B) REGISTRATION NUMBER: 28,029
 - (C) REFERENCE/DOCKET NUMBER: 514429-3647
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212-588-0800
 - (B) TELEFAX: 212-588-0500

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGGGCCACG GGATGACGCC TCCTCCGCCC GGACGTGCCG CCCCAGCGC ACCGCGCGCC	60
CGCGTCCCTG GCCCGCCGGC TCGGTTGGGG CTTCCGCTGC GGCTGCGGCT GCTGCTGCTG	120
CTCTGGGCGG CCGCCGCCTC CGCCAGGGC CACCTAAGGA GCGGACCCCG CATCTTCGCC	180
GTCTGGAAAG GCCATGTAGG GCAGGACCGG GTGGACTTTG GCCAGACTGA GCCGCACACG	240
GTGCTTTTCC ACGAGCCAGG CAGCTCCTCT GTGTGGGTGG GAGGACGTGG CAAGGTCTAC	300
CTCTTTGACT TCCCCGAGGG CAAGAACGCA TCTGTGCGCA CGGTGAATAT CGGCTCCACA	360
AAGGGGTCCT GTCTGGATAA GCGGGACTGC GAGAACTACA TCACTCTCCT GGAGAGGCGG	420
AGTGAGGGGC TGCTGGCCTG TGGCACCAAC GCCCGGCACC CCAGCTGCTG GAACCTGGTG	480
AATGGCACTG TGGTGCCACT TGGCGAGATG AGAGGCTACG CCCCCTTCAG CCCGGACGAG	540
AACTCCCTGG TTCTGTTTGA AGGGGACGAG GTGTATTCCA CCATCCGGAA GCAGGAATAC	600
AATGGGAAGA TCCCTCGGTT CCGCCGCATC CGGGGCGAGA GTGAGCTGTA CACCAGTGAT	660
ACTGTCATGC AGAACCACCA GTTCATCAAA GCCACCATCG TGCACCAAGA CCAGGCTTAC	720
GATGACAAGA TCTACTACTT CTTCCGAGAG GACAATCCTG ACAAGAATCC TGAGGCTCCT	780
CTCAATGTGT CCCGTGTGGC CCAGTTGTGC AGGGGGGACC AGGGTGGGGA AAGTTCACTG	840
TCAGTCTCCA AGTGGAACAC TTTTCTGAAA GCCATGCTGG TATGCAGTGA TGCTGCCACC	900
AACAAGAACT TCAACAGGCT GCAAGACGTC TTCCTGCTCC CTGACCCAG CGGCCAGTGG	960
AGGGACACCA GGGTCTATGG TGTTTTCTCC AACCCTGGA ACTACTCAGC CGTCTGTGTG	1020
TATTCCCTCG GTGACATTGA CAAGGTCTTC CGTACCTCCT CACTCAAGGG CTACCACTCA	1080
AGCCTTCCCA ACCCGCGGCC TGGCAAGTGC CTCCAGACC AGCAGCCGAT ACCCACAGAG	1140
ACCTTCCAGG TGGCTGACCG TCACCCAGAG GTGGCGCAGA GGGTGGAGCC CATGGGGCCT	1200
CTGAAGACGC CATTGTTCCA CTCTAAATAC CACTACCAGA AAGTGGCCGT TCACCGCATG	1260
CAAGCCAGCC ACGGGGAGAC CTTTCATGTG CTTTACCTAA CTACAGACAG GGGCACTATC	1320
CACAAGGTGG TGGAACCGGG GGAGCAGGAG CACAGCTTCG CCTTCAACAT CATGGAGATC	1380
CAGCCCTTCC GCCGCGCGGC TGCCATCCAG ACCATGTCGC TGGATGCTGA GCGGAGGAAG	1440
CTGTATGTGA GCTCCAGTG GGAGGTGAGC CAGGTGCCCC TGGACCTGTG TGAGGTCTAT	1500
GGCGGGGGCT GCCACGGTTG CCTCATGTCC CGAGACCCCT ACTGCGGCTG GGACCAGGGC	1560
CGCTGCATCT CCATCTACAG CTCCGAACGG TCAGTGCTGC AATCCATTAA TCCAGCCGAG	1620
CCACACAAGG AGTGTCCCAA CCCCAAACCA GACAAGGCC CACTGCAGAA GGTTTCCCTG	1680
GCCCCAACT CTCGCTACTA CCTGAGCTGC CCCATGGAAT CCCGCCACGC CACCTACTCA	1740

TGGCGCCACA AGGAGAACGT GGAGCAGAGC TGCGAACCTG GTCACCAGAG CCCCAACTGC 1800
 ATCCTGTTCA TCGAGAACCT CACGGCGCAG CAGTACGGCC ACTACTTCTG CGAGGCCAG 1860
 GAGGGCTCCT ACTTCCGCGA GGCTCAGCAC TGGCAGCTGC TGCCCGAGGA CGGCATCATG 1920
 GCCGAGCACC TGCTGGGTCA TGCCTGTGCC CTGGCTGCCT CCCTCTGGCT GGGGGTGCTG 1980
 CCCACACTCA CTCTTGGCTT GCTGGTCCAC TAGGGCCTCC CGAGGCTGGG CATGCCTCAG 2040
 GCTTCTGCAG CCCAGGGCAC TAGAACGTCT CACACTCAGA GCCGGCTGGC CCGGGAGCTC 2100
 CTTGCTGCC ACTTCTTCCA GGGGACAGAA TAACCCAGTG GAGGATGCCA GGCCTGGAGA 2160
 CGTCCAGCCG CAGGCGGCTG CTGGGCCCCA GGTGGCGCAC GGATGGTGAG GGGCTGAGAA 2220
 TGAGGGCACC GACTGTGAAG CTGGGGCATC GATGACCCAA GACTTTATCT TCTGGAAAAT 2280
 ATTTTTCAGA CTCCTCAAAC TTGACTAAAT GCAGCGATGC TCCAGCCCA AGAGCCCATG 2340
 GGTCGGGGAG TGGGTTTGGA TAGGAGAGCT GGGACTCCAT CTCGACCCTG GGGCTGAGGC 2400
 CTGAGTCCTT CTGGACTCTT GGTACCCACA TTGCCTCCTT CCCCTCCCTC TCTCATGGCT 2460
 GGGTGGCTGG TGTTCCTGAA GACCCAGGGC TACCCTCTGT CCAGCCCTGT CCTCTGCAGC 2520
 TCCCTCTCTG GTCCTGGGTC CCACAGGACA GCCGCCTTGC ATGTTTATTG AAGGATGTTT 2580
 GCTTCCCGGA CGGAAGGACG GAAAAAGCTC TGAAAAAAA AAAAAAAAAA AAAAAA 2636

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGGGCTGCG GGATGACGCC TCCTCCTCCC GGACGTGCCG CCCCCAGCGC ACCGCGCGCC 60
 CGCGTCCTCA GCCTGCCCGC TCGGTTGCGG CTCCCGCTGC GGCTGCGGCT TCTGCTGGTG 120
 TTCTGGGTGG CCGCCGCCTC CGCCCAAGGC CACTCGAGGA GCGGACCCCG CATCTCCGCC 180
 GTCTGGAAG GGCAGGACCA TGTGGACTTT AGCCAGCCTG AGCCACACAC CGTGCTTTTC 240
 CATGAGCCGG GCAGCTTCTC TGTCTGGGTG GGTGGACGTG GCAAGGTCTA CCACTTCAAC 300
 TTCCCCGAGG GCAAGAATGC CTCTGTGCGC ACGGTGAACA TCGGCTCCAC AAAGGGGTCC 360

TGTCAGGACA AACAGGACTG TGGGAATTAC ATCACTCTTC TAGAAAGGCG GGGTAATGGG 420
 CTGCTGGTCT GTGGCACCAA TGCCCGGAAG CCCAGCTGCT GGAACCTGGT GAATGACAGT 480
 GTGGTGATGT CACTTGGTGA GATGAAAGGC TATGCCCCCT TCAGCCCGGA TGAGAACTCC 540
 CTGGTTCTGT TTGAAGGAGA TGAAGTGAC TCTACCATCC GGAAGCAGGA ATACAACGGG 600
 AAGATCCCTC GGTTCGACG CATTCGGGGC GAGAGTGAAC TGTACACAAG TGATACAGTC 660
 ATGCAGAAC CACAGTTCAT CAAGGCCACC ATTGTGCACC AAGACCAAGC CTATGATGAT 720
 AAGATCTACT ACTTCTTCCG AGAAGACAAC CCTGACAAGA ACCCCGAGGC TCCTCTCAAT 780
 GTGTCCCGAG TAGCCAGTT GTGCAGGGGG GACCAGGGTG GTGAGAGTTC GTTGTCTGTC 840
 TCCAAGTGGA ACACCTTCCT GAAAGCCATG TTGGTCTGCA GCGATGCAGC CACCAACAGG 900
 AACTTCAATC GGCTGCAAGA TGTCTTCCTG CTCCCTGACC CCAGTGGCCA GTGGAGAGAT 960
 ACCAGGGTCT ATGGCGTTTT CTCCAACCCC TGGAAGTACT CAGCTGTCTG CGTGTATTCG 1020
 CTTGGTGACA TTGACAGAGT CTTCCTGACC TCATCGCTCA AAGGCTACCA CATGGGCCTT 1080
 TCCAACCCTC GACCTGGCAT GTGCCTCCCA AAAAAGCAGC CCATACCCAC AGAAACCTTC 1140
 CAGGTAGCTG ATAGTCACCC AGAGGTGGCT CAGAGGGTGG AACCTATGGG GCCCC 1195

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: n/a
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Pro Pro Pro Pro Gly Arg Ala Ala Pro Ser Ala Pro Arg Ala
 1 5 10 15
 Arg Val Pro Gly Pro Pro Ala Arg Leu Gly Leu Pro Leu Arg Leu Arg
 20 25 30
 Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu
 35 40 45
 Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln
 50 55 60
 Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His

65					70					75				80	
Glu	Pro	Gly	Ser	Ser	Ser	Val	Trp	Val	Gly	Gly	Arg	Gly	Lys	Val	Tyr
				85					90					95	
Leu	Phe	Asp	Phe	Pro	Glu	Gly	Lys	Asn	Ala	Ser	Val	Arg	Thr	Val	Asn
			100					105					110		
Ile	Gly	Ser	Thr	Lys	Gly	Ser	Cys	Leu	Asp	Lys	Arg	Asp	Cys	Glu	Asn
		115					120					125			
Tyr	Ile	Thr	Leu	Leu	Glu	Arg	Arg	Ser	Glu	Gly	Leu	Leu	Ala	Cys	Gly
	130					135					140				
Thr	Asn	Ala	Arg	His	Pro	Ser	Cys	Trp	Asn	Leu	Val	Asn	Gly	Thr	Val
145					150					155				160	
Val	Pro	Leu	Gly	Glu	Met	Arg	Gly	Tyr	Ala	Pro	Phe	Ser	Pro	Asp	Glu
			165						170					175	
Asn	Ser	Leu	Val	Leu	Phe	Glu	Gly	Asp	Glu	Val	Tyr	Ser	Thr	Ile	Arg
		180						185					190		
Lys	Gln	Glu	Tyr	Asn	Gly	Lys	Ile	Pro	Arg	Phe	Arg	Arg	Ile	Arg	Gly
	195						200						205		
Glu	Ser	Glu	Leu	Tyr	Thr	Ser	Asp	Thr	Val	Met	Gln	Asn	Pro	Gln	Phe
	210					215					220				
Ile	Lys	Ala	Thr	Ile	Val	His	Gln	Asp	Gln	Ala	Tyr	Asp	Asp	Lys	Ile
225					230					235					240
Tyr	Tyr	Phe	Phe	Arg	Glu	Asp	Asn	Pro	Asp	Lys	Asn	Pro	Glu	Ala	Pro
			245						250					255	
Leu	Asn	Val	Ser	Arg	Val	Ala	Gln	Leu	Cys	Arg	Gly	Asp	Gln	Gly	Gly
		260						265					270		
Glu	Ser	Ser	Leu	Ser	Val	Ser	Lys	Trp	Asn	Thr	Phe	Leu	Lys	Ala	Met
		275					280					285			
Leu	Val	Cys	Ser	Asp	Ala	Ala	Thr	Asn	Lys	Asn	Phe	Asn	Arg	Leu	Gln
	290					295					300				
Asp	Val	Phe	Leu	Leu	Pro	Asp	Pro	Ser	Gly	Gln	Trp	Arg	Asp	Thr	Arg
305					310					315					320
Val	Tyr	Gly	Val	Phe	Ser	Asn	Pro	Trp	Asn	Tyr	Ser	Ala	Val	Cys	Val
			325						330					335	
Tyr	Ser	Leu	Gly	Asp	Ile	Asp	Lys	Val	Phe	Arg	Thr	Ser	Ser	Leu	Lys
		340						345					350		
Gly	Tyr	His	Ser	Ser	Leu	Pro	Asn	Pro	Arg	Pro	Gly	Lys	Cys	Leu	Pro
	355						360					365			
Asp	Gln	Gln	Pro	Ile	Pro	Thr	Glu	Thr	Phe	Gln	Val	Ala	Asp	Arg	His

370	375	380
Pro Glu Val Ala Gln Arg Val Glu Pro Met Gly Pro Leu Lys Thr Pro		
385	390	400
Leu Phe His Ser Lys Tyr His Tyr Gln Lys Val Ala Val His Arg Met		
405	410	415
Gln Ala Ser His Gly Glu Thr Phe His Val Leu Tyr Leu Thr Thr Asp		
420	425	430
Arg Gly Thr Ile His Lys Val Val Glu Pro Gly Glu Gln Glu His Ser		
435	440	445
Phe Ala Phe Asn Ile Met Glu Ile Gln Pro Phe Arg Arg Ala Ala Ala		
450	455	460
Ile Gln Thr Met Ser Leu Asp Ala Glu Arg Arg Lys Leu Tyr Val Ser		
465	470	475
Ser Gln Trp Glu Val Ser Gln Val Pro Leu Asp Leu Cys Glu Val Tyr		
485	490	495
Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly		
500	505	510
Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val		
515	520	525
Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro		
530	535	540
Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser		
545	550	555
Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser		
565	570	575
Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln		
580	585	590
Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr		
595	600	605
Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala		
610	615	620
Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu		
625	630	635
Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu		
645	650	655
Pro Thr Leu Thr Leu Gly Leu Leu Val His		
660	665	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: n/a

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Pro Pro Pro Gly Arg Ala Ala Pro Ser Ala Pro Arg Ala
1 5 10 15

Arg Val Leu Ser Leu Pro Ala Arg Phe Gly Leu Pro Leu Arg Leu Arg
20 25 30

Leu Leu Leu Val Phe Trp Val Ala Ala Ala Ser Ala Gln Gly His Ser
35 40 45

Arg Ser Gly Pro Arg Ile Ser Ala Val Trp Lys Gly Gln Asp His Val
50 55 60

Asp Phe Ser Gln Pro Glu Pro His Thr Val Leu Phe His Glu Pro Gly
65 70 75 80

Ser Phe Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr His Phe Asn
85 90 95

Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn Ile Gly Ser
100 105 110

Thr Lys Gly Ser Cys Gln Asp Lys Gln Asp Cys Gly Asn Tyr Ile Thr
115 120 125

Leu Leu Glu Arg Arg Gly Asn Gly Leu Leu Val Cys Gly Thr Asn Ala
130 135 140

Arg Lys Pro Ser Cys Trp Asn Leu Val Asn Asp Ser Val Val Met Ser
145 150 155 160

Leu Gly Glu Met Lys Gly Tyr Ala Pro Phe Ser Pro Asp Glu Asn Ser
165 170 175

Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg Lys Gln
180 185 190

Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly Glu Ser
195 200 205

Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe Ile Lys
210 215 220

Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile Tyr Tyr

225 230 235 240
 Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro Leu Asn
 245 250 255
 Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly Glu Ser
 260 265 270
 Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met Leu Val
 275 280 285
 Cys Ser Asp Ala Ala Thr Asn Arg Asn Phe Asn Arg Leu Gln Asp Val
 290 295 300
 Phe Leu Leu Pro Asp Pro Ser Gly Gln Trp Arg Asp Thr Arg Val Tyr
 305 310 315 320
 Gly Val Phe Ser Asn Pro Trp Asn Tyr Ser Ala Val Cys Val Tyr Ser
 325 330 335
 Leu Gly Asp Ile Asp Arg Val Phe Arg Thr Ser Ser Leu Lys Gly Tyr
 340 345 350
 His Met Gly Leu Ser Asn Pro Arg Pro Gly Met Cys Leu Pro Lys Lys
 355 360 365
 Gln Pro Ile Pro Thr Glu Thr Phe Gln Val Ala Asp Ser His Pro Glu
 370 375 380
 Val Ala Gln Arg Val Glu Pro Met Gly Pro
 385 390

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCCGCACAC GGTGCTTTTC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCACAGATGC GTTCTTGCCC

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACCATAGACC CTGGTGTCCC

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCAGTGATGC TGCCACCAAC

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAGACCATG TCGCTGGATG

20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACATGAGGCA ACCGTGGCAG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGTAGACCT TGCCACGTCC

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAACTTCAAC AGGCTGCAAG ACG

23

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGCTGAGCG GAGGAAGCTG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGCCATACA CCTCACACAG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGGAAGCTT TCTGTGGGTA TCGGCTGC

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGGATCCC TGGTTCTGTT TGAAG

25

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTCTAGAATT CAGCGGCCGC TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGGAAAGTT CACTGTCAGT CTCCAAG

27

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGAATACAC ACAGACGGCT GAGTAG

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCAAGTTCA GCCTGGTTAA GT

22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTATGAGTAT TTCTTCCAGG G

21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATTAATCC AGCCGAGCCA CACAAG

26

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CATCTACAGC TCCGAACGGT CAGTG

25

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGCGGAAGC CCCAACCGAG

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGATGACGC CTCCTCCGCC CGG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTTCACG TGGACCAGCA AGCCAAGAGT G

31

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGCTTTTTTC CGTCCTTCCG TCCGG

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGTGAGCA AGGGCGAGGA GCTG

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTTGTCAGC TCGTCCATGC CGAG

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGTGGTGAG AGTTCGTTGT CTGTC

25

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAGCGATGAG GTACGGAAGA CTCTG

25

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5856 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TGCAGCTGGC	60
ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC	120
TCACTCATTG GGCACCCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA	180
TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTTC	240
ACGTGGACCA GCAAGCCAAG AGTGAGTGTG GGCAGCACCC CCAGCCAGAG GGAGGCAGCC	300
AGGGCACAGG CATGACCCAG CAGGTGCTCG GCCATGATGC CGTCCCTCGGG CAGCAGCTGC	360
CAGTGCTGAG CCTCGCGGAA GTAGGAGCCC TCCTGGGCCT CGCAGAAGTA GTGGCCGTAC	420
TGCTGCGCCG TGAGGTTCTC GATGAACAGG ATGCAGTTGG GGCTCTGGTG ACCAGGTTTCG	480
CAGCTCTGCT CCACGTTCTC CTTGTGGCGC CATGAGTAGG TGGCGTGGCG GGATTCCATG	540
GGGCAGCTCA GGTAGTAGCG AGAGTTTGGG GCCAGGGAAA CCTTCTGCAG TGGGGCCTTG	600
TCTGGTTTGG GGTGGGACA CTCCTTGTGT GGCTCGGCTG GATTAATGGA TTGCAGCACT	660
GACCGTTCGG AGCTGTAGAT GGAGATGCAG CGGCCCTGGT CCCAGCCGCA GTAGGGGTCT	720
CGGGACATGA GGCAACCGTG GCAGCCCCCG CCATAGACCT CACACAGGTC CAGGGGCACC	780
TGGCTCACCT CCCACTGGGA GCTCACATAC AGCTTCCTCC GCTCAGCATC CAGCGACATG	840
GTCTGGATGG CAGCCGCGCG GCGGAAGGGC TGGATCTCCA TGATGTTGAA GGCGAAGCTG	900

TCGGTCGCCG GGC GCGGTAT TCTCAGAATG ACTTGGTTGA GTACTCACCA GTCACAGAAA	4380
AGCATCTTAC GGATGGCATG ACAGTAAGAG AATTATGCAG TGCTGCCATA ACCATGAGTG	4440
ATAAACTGTC GGCCAACTTA CTTCTGACAA CGATCGGAGG ACCGAAGGAG CTAACCGCTT	4500
TTTTGCACAA CATGGGGGAT CATGTAACTC GCCTTGATCG TTGGGAACCG GAGCTGAATG	4560
AAGCCATACC AAACGACGAG AGTGACACCA CGATGCCTGT AGCAATGCCA ACAACGTTGC	4620
GCAAACTATT AACTGGCGAA CTACTTACTC TAGCTTCCCG GCAACAATTA ATAGACTGGA	4680
TGGAGGCGGA TAAAGTTGCA GGACCACTTC TGCCTCGGC CCTTCCGGCT GGCTGGTTTA	4740
TTGCTGATAA ATCTGGAGCC GGTGAGCGTG GGTCTCGCGG TATCATTGCA GCACTGGGGC	4800
CAGATGGTAA GCCCTCCCGT ATCGTAGTTA TCTACACGAC GGGGAGTCAG GCAACTATGG	4860
ATGAACGAAA TAGACAGATC GCTGAGATAG GTGCCTCACT GATTAAGCAT TGGTAACTGT	4920
CAGACCAAGT TTACTCATAT ATACTTTAGA TTGATTTAAA ACTTCATTTT TAATTTAAAA	4980
GGATCTAGGT GAAGATCCTT TTTGATAATC TCATGACCAA AATCCCTTAA CGTGAGTTTT	5040
CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA GATCCTTTTT	5100
TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG GTGGTTTGTT	5160
TGCCGGATCA AGAGCTACCA ACTCTTTTTTC CGAAGGTAAC TGGCTTCAGC AGAGCGCAGA	5220
TACCAAATAC TGTCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG AACTCTGTAG	5280
CACCGCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC AGTGGCGATA	5340
AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG CAGCGGTCGG	5400
GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC ACCGAACTGA	5460
GATACCTACA GCGTGAGCAT TGAGAAAGCG CCACGCTTCC CGAAGGGAGA AAGGCGGACA	5520
GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT CCAGGGGGAA	5580
ACGCCTGGTA TCTTTATAGT CCTGTGCGGT TTCGCCACCT CTGACTTGAG CGTCGATTTT	5640
TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG GCCTTTTAC	5700
GGTTCCTGGC CTTTTGCTGG CCITTTGCTC ACATGTTCTT TCCTGCGTTA TCCCCTGATT	5760
CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC AGCCGAACGA	5820
CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAG	5856

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID: NO: 35:

GACGGATCGG GAGATCTCCC GATCCCCTAT GGTGACTCT CAGTACAATC TGCTCTGATG 60
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG 120
CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC 180
TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT 240
GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA 300
TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC 360
CCCGCCCAT T GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC 420
ATTGACGTCA ATGGGTGGAC TATTTACGGT AAATGCCCCA CTTGGCAGTA CATCAAGTGT 480
ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT 540
ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA 600
TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG 660
ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC 720
AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG 780
GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA 840
CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC 900
GTTTAAACGG GCCCTCTAGA CTCGAGCGGC CGCCACTGTG CTGGATATCT GCAGAAATCG 960
GCTTGGGATG ACGCCTCCTC CGCCCGGACG TGCCGCCCCC AGCGCACCGC GCGCCCGCGT 1020
CCCTGGCCCG CCGGCTCGGT TGGGGCTTCC GCTGCGGCTG CGGCTGCTGC TGCTGCTCTG 1080
GGCGGCCGCC GCCTCCGCCC AGGGCCACCT AAGGAGCGGA CCCC GCATCT TCGCCGCTCTG 1140
GAAAGGCCAT GTAGGGCAGG ACCGGGTGGA CTTTGGCCAG ACTGAGCCGC ACACGGTGCT 1200
TTCCACGAG CCAGGCAGCT CCTCTGTGTG GGTGGGAGGA CGTGGCAAGG TCTACCTCTT 1260
TGACTTCCCC GAGGGCAAGA ACGCATCTGT GCGCACGGTG AATATCGGCT CCACAAAGGG 1320
GTCCTGTCTG GATAAGCGGG ACTGCGAGAA CTACATCACT CTCCTGGAGA GGCGGAGTGA 1380
GGGGCTGCTG GCCTGTGGCA CCAACGCCCG GCACCCAGC TGCTGGAACC TGGTGAATGG 1440

TCCTTGACCC	TGGAAGGTGC	CACTCCCCT	GTCCTTTTCT	AATAAAATGA	GGAAATTGCA	3180
TCGCATTGTC	TGAGTAGGTG	TCATTCTATT	CTGGGGGGTG	GGGTGGGGCA	GGACAGCAAG	3240
GGGGAGGATT	GGGAAGACAA	TAGCAGGCAT	GCTGGGGATG	CGGTGGGCTC	TATGGCTTCT	3300
GAGGCGGAAA	GAACCAGCTG	GGGCTCTAGG	GGGTATCCCC	ACGCGCCCTG	TAGCGGCGCA	3360
TTAAGCGCGG	CGGGTGTGGT	GGTTACGCGC	AGCGTGACCG	CTACACTTGC	CAGCGCCCTA	3420
GCGCCCGCTC	CTTTCGCTTT	CTTCCCTTCC	TTTCTCGCCA	CGTTCGCCGG	CTTTCCCCGT	3480
CAAGCTCTAA	ATCGGGGCAT	CCCTTTAGGG	TTCCGATTTA	GTGCTTTACG	GCACCTCGAC	3540
CCCCAAAAAC	TTGATTAGGG	TGATGGTTCA	CGTAGTGGGC	CATCGCCCTG	ATAGACGGTT	3600
TTTCGCCCTT	TGACGTTGGA	GTCCACGTTT	TTTAATAGTG	GACTCTTGTT	CCAAACTGGA	3660
ACAACACTCA	ACCCTATCTC	GGTCTATTCT	TTTGATTTAT	AAGGGATTTT	GGGGATTTTCG	3720
GCCTATTGGT	TAAAAAATGA	GCTGATTTAA	CAAAAATTTA	ACGCGAATTA	ATTCTGTGGA	3780
ATGTGTGTCA	GTTAGGGTGT	GGAAAGTCCC	CAGGCTCCCC	AGGCAGGCAG	AAGTATGCAA	3840
AGCATGCATC	TCAATTAGTC	AGCAACCAGG	TGTGGAAAGT	CCCCAGGCTC	CCAGCAGGC	3900
AGAAGTATGC	AAAGCATGCA	TCTCAATTAG	TCAGCAACCA	TAGTCCCGCC	CCTAACTCCG	3960
CCCATCCCGC	CCCTAACTCC	GCCCAGTTCC	GCCCATTCTC	CGCCCCATGG	CTGACTAATT	4020
TTTTTTATTT	ATGCAGAGGC	CGAGGCCGCC	TCTGCCTCTG	AGCTATTCCA	GAAGTAGTGA	4080
GGAGGCTTTT	TTGGAGGCCT	AGGCTTTTGC	AAAAAGCTCC	CGGGAGCTTG	TATATCCATT	4140
TTCGGATCTG	ATCAAGAGAC	AGGATGAGGA	TCGTTTCGCA	TGATTGAACA	AGATGGATTG	4200
CACGCAGGTT	CTCCGGCCGC	TTGGGTGGAG	AGGCTATTCC	GCTATGACTG	GGCACAACAG	4260
ACAATCGGCT	GCTCTGATGC	CGCCGTGTTT	CGGCTGTCAG	CGCAGGGGCG	CCCGGTTCTT	4320
TTTGTCAAGA	CCGACCTGTC	CGGTGCCCTG	AATGAACTGC	AGGACGAGGC	AGCGCGGCTA	4380
TCGTGGCTGG	CCACGACGGG	CGTTCCTTGC	GCAGCTGTGC	TCGACGTTGT	CACTGAAGCG	4440
GGAAAGGACT	GGCTGCTATT	GGGCGAAGTG	CCGGGGCAGG	ATCTCCTGTC	ATCTCACCTT	4500
GCTCCTGCCG	AGAAAGTATC	CATCATGGCT	GATGCAATGC	GGCGGCTGCA	TACGCTTGAT	4560
CCGGCTACCT	GCCCATTCTG	CCACCAAGCG	AAACATCGCA	TCGAGCGAGC	ACGTACTCGG	4620
ATGGAAGCCG	GTCTTGTCGA	TCAGGATGAT	CTGGACGAAG	AGCATCAGGG	GCTCGCGCCA	4680
GCCGAAGTGT	TCGCCAGGCT	CAAGGCGCGC	ATGCCCCGAC	GCGAGGATCT	CGTCGTGACC	4740
CATGGCGATG	CCTGCTTGCC	GAATATCATG	GTGGAAAATG	GCCGCTTTTC	TGGATTTCATC	4800
GACTGTGGCC	GGCTGGGTGT	GGCGGACCGC	TATCAGGACA	TAGCGTTGGC	TACCCGTGAT	4860

ATTGCTGAAG AGCTTGGCGG CGAATGGGCT GACCGCTTCC TCGTGCTTTA CGGTATCGCC	4920
GCTCCCGATT CGCAGCGCAT CGCCTTCTAT CGCCTTCTTG ACGAGTTCTT CTGAGCGGGA	4980
CTCTGGGGTT CGAAATGACC GACCAAGCGA CGCCCAACCT GCCATCACGA GATTTTCGATT	5040
CCACCGCCGC CTTCTATGAA AGGTGGGCT TCGGAATCGT TTTCCGGGAC GCCGGCTGGA	5100
TGATCCTCCA GCGCGGGGAT CTCATGCTGG AGTTCTTCGC CCACCCCAAC TTGTTTATTG	5160
CAGCTTATAA TGGTTACAAA TAAAGCAATA GCATCACAAA TTTCACAAAT AAAGCATTTT	5220
TTTCACTGCA TTCTAGTTGT GGTTTGTCCA AACTCATCAA TGTATCTTAT CATGTCTGTA	5280
TACCGTCGAC CTCTAGCTAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA	5340
ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCT	5400
GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTC	5460
AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG	5520
GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTT	5580
GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG	5640
GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA	5700
AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC	5760
GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC	5820
CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG	5880
CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT	5940
CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC	6000
GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC	6060
CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG	6120
AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG	6180
CTCTGCTGAA GCCAGTTACC TTGGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA	6240
CCACCGCTGG TAGCGGTGGT TTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAG	6300
GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAACT	6360
CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA	6420
ATTAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT	6480
ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTTCGT TCATCCATAG	6540

TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA	6600
GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC	6660
AGCCAGCCGG AAGGGCCGAG CGCAGAAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT	6720
CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG	6780
TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA	6840
GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG	6900
TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA	6960
TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG	7020
TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT	7080
CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA	7140
TCATTGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA	7200
GTTCGATGTA ACCCACTCGT GCACCCAAC TATCTTCAGC ATCTTTTACT TTCACCAGCG	7260
TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAA AAAGGGAATA AGGGCGACAC	7320
GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT	7380
ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC	7440
CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTC	7475

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GACGGATCGG GAGATCTCCC GATCCCCTAT GGTGCACTCT CAGTACAATC TGCTCTGATG	60
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG	120
CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC	180
TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT	240
GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA	300

TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCCGCC TGGCTGACCG CCCAACGACC	360
CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC	420
ATTGACGTCA ATGGGTGGAC TATTTACGGT AAAGTGGCCA CTTGGCAGTA CATCAAGTGT	480
ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT	540
ATGCCCAGTA CATGACCTTA TGGGACTTTC CTAAGTGGCA GTACATCTAC GTATTAGTCA	600
TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG	660
ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC	720
AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG	780
GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA	840
CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC	900
GTTTAAACGG GCCCTCTAGA CTCGAGCGGC CGCCACTGTG CTGGATATCT GCAGAATTCG	960
GCTTGGGATG ACGCCTCCTC CGCCCGGACG TGCCGCCCCC AGCGCACCGC GCGCCCGCGT	1020
CCCTGGCCCC CGGCTCGGT TGGGGCTTCC GCTGCGGCTG CGGCTGCTGC TGCTGCTCTG	1080
GGCGGCCGCC GCCTCCGCCC AGGGCCACCT AAGGAGCGGA CCCC GCATCT TCGCCGTCTG	1140
GAAAGGCCAT GTAGGGCAGG ACCGGGTGGA CTTTGGCCAG ACTGAGCCGC ACACGGTGCT	1200
TTTCCACGAG CCAGGCAGCT CCTCTGTGTG GGTGGGAGGA CGTGGCAAGG TCTACCTCTT	1260
TGACTTCCCC GAGGGCAAGA ACGCATCTGT GCGCACGGTG AATATCGGCT CCACAAAGGG	1320
GTCTGTCTG GATAAGCGGG ACTGCGAGAA CTACATCACT CTCCTGGAGA GCGGAGTGA	1380
GGGGCTGCTG GCCTGTGGCA CCAACGCCCC GCACCCAGC TGCTGGAACC TGGTGAATGG	1440
CACTGTGGTG CCACTTGGCG AGATGAGAGG CTACGCCCCC TTCAGCCCGG ACGAGAACTC	1500
CCTGGTTCTG TTTGAAGGGG ACGAGGTGTA TTCCACCATC CGGAAGCAGG AATACAATGG	1560
GAAGATCCCT CGGTTCCGCC GCATCCGGGG CGAGAGTGAG CTGTACACCA GTGATACTGT	1620
CATGCAGAAC CCACAGTTCA TCAAAGCCAC CATCGTGCAC CAAGACCAGG CTTACGATGA	1680
CAAGATCTAC TACTTCTTCC GAGAGGACAA TCCTGACAAG AATCCTGAGG CTCCTCTCAA	1740
TGTGTCCCGT GTGGCCCAGT TGTGCAGGGG GGACCAGGGT GGGGAAAGTT CACTGTCACT	1800
CTCCAAGTGG AACACTTTTC TGAAAGCCAT GCTGGTATGC AGTGATGCTG CCACCAACAA	1860
GAAGTTCAAC AGGCTGCAAG ACGTCTTCCT GCTCCCTGAC CCCAGCGGCC AGTGGAGGGA	1920
CACCAGGGTC TATGGTGTTT TCTCCAACCC CTGGAAGTAC TCAGCCGTCT GTGTGTATTC	1980
CCTCGGTGAC ATTGACAAGG TCTTCCGTAC CTCCTCACTC AAGGGCTACC ACTCAAGCCT	2040

TCCCAACCCG	CGGCCTGGCA	AGTGCCTCCC	AGACCAGCAG	CCGATACCCA	CAGAGACCTT	2100
CCAGGTGGCT	GACCGTCACC	CAGAGGTGGC	GCAGAGGGTG	GAGCCCATGG	GGCCTCTGAA	2160
GAGCCCATTG	TTCCACTCTA	AATACCACTA	CCAGAAAGTG	GCCGTTTACC	GCATGCAAGC	2220
CAGCCACGGG	GAGACCTTTC	ATGTGCTTTA	CCTAACTACA	GACAGGGGCA	CTATCCACAA	2280
GGTGGTGGAA	CCGGGGGAGC	AGGAGCACAG	CTTCGCCTTC	AACATCATGG	AGATCCAGCC	2340
CTTCCGCCGC	GCGGCTGCCA	TCCAGACCAT	GTCGCTGGAT	GCTGAGCGGA	GGAAGCTGTA	2400
TGTGAGCTCC	CAGTGGGAGG	TGAGCCAGGT	GCCCCTGGAC	CTGTGTGAGG	TCTATGGCGG	2460
GGGCTGCCAC	GGTTGCCCTCA	TGTCCCGAGA	CCCCTACTGC	GGCTGGGACC	AGGGCCGCTG	2520
CATCTCCATC	TACAGCTCCG	AACGGTCAGT	GCTGCAATCC	ATTAATCCAG	CCGAGCCACA	2580
CAAGGAGTGT	CCCAACCCCA	AACCAGACAA	GGCCCCACTG	CAGAAGGTTT	CCCTGGCCCC	2640
AAACTCTCGC	TACTACCTGA	GCTGCCCCAT	GGAATCCCGC	CACGCCACCT	ACTCATGGCG	2700
CCACAAGGAG	AACGTGGAGC	AGAGCTGCGA	ACCTGGTCAC	CAGAGCCCCA	ACTGCATCCT	2760
GTTCATCGAG	AACCTCACGG	CGCAGCAGTA	CGGCCACTAC	TTCTGCGAGG	CCCAGGAGGG	2820
CTCCTACTTC	CGCGAGGCTC	AGCACTGGCA	GCTGCTGCCC	GAGGACGGCA	TCATGGCCGA	2880
GCACCTGCTG	GGTCATGCCT	GTGCCCTGGC	TGCCTCCCTC	TGGCTGGGGG	TGCTGCCCCAC	2940
ACTCACTCTT	GGCTTGCTGG	TCCACATGGT	GAGCAAGGGC	GAGGAGCTGT	TCACCGGGGT	3000
GGTGCCCATC	CTGGTCGAGC	TGGACGGCGA	CGTAAACGGC	CACAAGTTCA	GCGTGTCCGG	3060
CGAGGGCGAG	GGCGATGCCA	CCTACGGCAA	GCTGACCCTG	AAGTTCATCT	GCACCACCGG	3120
CAAGCTGCCC	GTGCCCTGGC	CCACCCTCGT	GACCACCCTG	ACCTACGGCG	TGCAGTGCTT	3180
CAGCCGCTAC	CCCGACCACA	TGAAGCAGCA	CGACTTCTTC	AAGTCCGCCA	TGCCCCGAAGG	3240
CTACGTCCAG	GAGCGCACCA	TCTTCTTCAA	GGACGACGGC	AACTACAAGA	CCCGCGCCGA	3300
GGTGAAGTTC	GAGGGCGACA	CCCTGGTGAA	CCGCATCGAG	CTGAAGGGCA	TCGACTTCAA	3360
GGAGGACGGC	AACATCCTGG	GGCACAAGCT	GGAGTACAAC	TACAACAGCC	ACAACGTCTA	3420
TATCATGGCC	GACAAGCAGA	AGAACGGCAT	CAAGGTGAAC	TTCAAGATCC	GCCACAACAT	3480
CGAGGACGGC	AGCGTGCAGC	TCGCCGACCA	CTACCAGCAG	AACACCCCCA	TCGGCGACGG	3540
CCCCGTGCTG	CTGCCCGACA	ACCACTACCT	GAGCACCCAG	TCCGCCCTGA	GCAAAGACCC	3600
CAACGAGAAG	CGCGATCACA	TGGTCCTGCT	GGAGTTCGTG	ACCGCCGCCG	GGATCACTCT	3660
CGGCATGGAC	GAGCTGTACA	AGGTGAAGCT	TGGGCCCCGA	CAAAAACCTCA	TCTCAGAAGA	3720

GGATCTGAAT	AGCGCCGTCG	ACCATCATCA	TCATCATCAT	TGAGTTTAAA	CCGCTGATCA	3780
GCCTCGACTG	TGCCTTCTAG	TTGCCAGCCA	TCTGTTGTTT	GCCCCCCCC	CGTGCCTTCC	3840
TTGACCCTGG	AAGGTGCCAC	TCCCACGTCT	CTTTCCTAAT	AAAATGAGGA	AATTGCATCG	3900
CATTGTCTGA	GTAGGTGTCA	TTCTATTCTG	GGGGGTGGGG	TGGGGCAGGA	CAGCAAGGGG	3960
GAGGATTGGG	AAGACAATAG	CAGGCATGCT	GGGGATGCGG	TGGGCTCTAT	GGCTTCTGAG	4020
GCGGAAAGAA	CCAGCTGGGG	CTCTAGGGGG	TATCCCCACG	CGCCCTGTAG	CGGCGCATT	4080
AGCGCGGCGG	GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CAC TTGCCAG	CGCCCTAGCG	4140
CCCGCTCCTT	TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT	TCCCCGTCAA	4200
GCTCTAAATC	GGGGCATCCC	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	4260
AAAAAACTTG	ATTAGGGTGA	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	4320
CGCCCTTTGA	CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	4380
AACTCAACC	CTATCTCGGT	CTATTCTTTT	GATTTATAAG	GGATTTTGGG	GATTTTCGGC	4440
TATTGGTTAA	AAAATGAGCT	GATTTAACAA	AAATTTAACG	CGAATTAATT	CTGTGGAATG	4500
TGTGTCAGTT	AGGGTGTGGA	AAGTCCCCAG	GCTCCCCAGG	CAGGCAGAAG	TATGCAAAGC	4560
ATGCATCTCA	ATTAGTCAGC	AACCAGGTGT	GGAAAGTCCC	CAGGCTCCCC	AGCAGGCAGA	4620
AGTATGCAAA	GCATGCATCT	CAATTAGTCA	GCAACCATAG	TCCCGCCCCCT	AACTCCGCCC	4680
ATCCCGCCCC	TAACTCCGCC	CAGTTCCGCC	CATTCTCCGC	CCCATGGCTG	ACTAATTTTT	4740
TTTATTTATG	CAGAGGCCGA	GGCCGCCTCT	GCCTCTGAGC	TATTCCAGAA	GTAGTGAGGA	4800
GGCTTTTTTG	GAGGCCTAGG	CTTTTGCAAA	AAGCTCCCGG	GAGCTTGTAT	ATCCATTTTC	4860
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ATCGGCTGCT	CTGATGCCGC	CGTGTTCCGG	CTGTACGCGC	AGGGGCGCCC	GGTTCTTTTT	5040
GTCAAGACCG	ACCTGTCCGG	TGCCCTGAAT	GAAGTGCAGG	ACGAGGCAGC	GCGGCTATCG	5100
TGGCTGGCCA	CGACGGGCGT	TCCTTGCGCA	GCTGTGCTCG	ACGTTGTCAC	TGAAGCGGGA	5160
AGGGACTGGC	TGCTATTGGG	CGAAGTGCCG	GGGCAGGATC	TCCTGTCATC	TCACCTTGCT	5220
CCTGCCGAGA	AAGTATCCAT	CATGGCTGAT	GCAATGCGGC	GGCTGCATAC	GCTTGATCCG	5280
GCTACCTGCC	CATTCGACCA	CCAAGCGAAA	CATCGCATCG	AGCGAGCACG	TACTCGGATG	5340
GAAGCCGGTC	TTGTCGATCA	GGATGATCTG	GACGAAGAGC	ATCAGGGGCT	CGCGCCAGCC	5400
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TGTGGCCGGC TGGGTGTGGC GGACCGCTAT CAGGACATAG CGTTGGCTAC CCGTGATATT	5580
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TGGGGTTTCGA AATGACCGAC CAAGCGACGC CCAACCTGCC ATCACGAGAT TTCGATTCCA	5760
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GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG CATAAAGTGT AAAGCCTGGG	6120
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CGGGAAACCT GTCGTGCCAG CTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT	6240
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GTAAAGGGAT TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT	7140

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 AATGTTGAAT ACTCATACTC TTCCTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT 8100
 GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC 8160
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(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGATCTCGGC CGCATATTAA GTGCATTGTT CTCGATACCG CTAAGTGCAT TGTTCTCGTT 60
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 TCTTGCTGAA AGCTCGATGG ACAAGTGCAT TGTTCTCTTG CTGAAAGCTC AGTACCCGGG 180

AGTACCCTCG ACCGCCGGAG TATAAATAGA GGCCTTCGT CTACGGAGCG ACAATTCAAT	240
TCAAACAAGC AAAGTGAACA CGTCGCTAAG CGAAAGCTAA GCAAATAAAC AAGCGCAGCT	300
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GAAGAGAACT CTGAATACTT TCAACAAGTT ACCGAGAAAG AAGAACTCAC ACACAGCTAG	480
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CCTGGCCCCG CGGCTCGGTT GGGGCTTCCG CTGCGGCTGC GGCTGCTGCT GCTGCTCTGG	660
GCGGCCCGCG CCTCCGCCCA GGGCCACCTA AGGAGCGGAC CCCGCATCTT CGCCGTCTGG	720
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GACTTCCCCG AGGGCAAGAA CGCATCTGTG CGCACGGTGA ATATCGGCTC CACAAAGGGG	900
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GGGCTGCTGG CCTGTGGCAC CAACGCCCCG CACCCAGCT GCTGGAACCT GGTGAATGGC	1020
ACTGTGGTGC CACTTGCGCA GATGAGAGGC TACGCCCCCT TCAGCCCGGA CGAGAACTCC	1080
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TCCAAGTGGA AACTTTTCT GAAAGCCATG CTGGTATGCA GTGATGCTGC CACCAACAAG	1440
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AACTCTCGCT	ACTACCTGAG	CTGCCCCATG	GAATCCCGCC	ACGCCACCTA	CTCATGGCGC	2280
CACAAGGAGA	ACGTGGAGCA	GAGCTGCGAA	CCTGGTCACC	AGAGCCCCAA	CTGCATCCTG	2340
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 GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG GGTATTGTC 6900
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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

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AGTACCCTCG ACCGCCGGAG TATAAATAGA GCGCCTTCGT CTACGGAGCG ACAATTCAAT 240
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GAACAAGCTA AACAACTCTG AGTAAAGTGC AAGTTAAAGT GAATCAATTA AAAGTAACCA 360
GCAACCAAGT AAATCAACTG CAACTACTGA AATCTGCCAA GAAGTAATTA TTGAATACAA 420
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TTCCGCCGCG CGGCTGCCAT CCAGACCATG TCGCTGGATG CTGAGCGGAG GAAGCTGTAT	1980
GTGAGCTCCC AGTGGGAGGT GAGCCAGGTG CCCCTGGACC TGTGTGAGGT CTATGGCGGG	2040
GGCTGCCACG GTTGCTCAT GTCCCGAGAC CCCTACTGCG GCTGGGACCA GGGCCGCTGC	2100
ATCTCCATCT ACAGCTCCGA ACGGTCAGTG CTGCAATCCA TTAATCCAGC CGAGCCACAC	2160
AAGGAGTGTC CCAACCCCAA ACCAGACAAG GCCCCACTGC AGAAGGTTTC CCTGGCCCCA	2220
AACTCTCGCT ACTACCTGAG CTGCCCCATG GAATCCCGCC ACGCCACCTA CTCATGGCGC	2280
CACAAGGAGA ACGTGGAGCA GAGCTGCGAA CCTGGTCACC AGAGCCCCAA CTGCATCCTG	2340
TTCATCGAGA ACCTCACGGC GCAGCAGTAC GGCCACTACT TCTGCGAGGC CCAGGAGGGC	2400
TCCTACTTCC GCGAGGCTCA GCACTGGCAG CTGCTGCCCC AGGACGGCAT CATGGCCGAG	2460
CACCTGCTGG GTCATGCCTG TGCCCTGGCT GCCTCCCTCT GGCTGGGGGT GCTGCCCACA	2520
CTCACTCTTG GCTTGCTGGT CCACGTGAAG CTTGGGCCCC AACAAAACT CATCTCAGAA	2580
GAGGATCTGA ATAGCGCCGT CGACCATCAT CATCATCATC ATTGAGTTTA TCCAGCACAG	2640
TGGCGGCCGC TCGAGTCTAG AGGGCCCCGT TAAACCCGCT GATCAGCCTC GACTGTGCCT	2700
TCTAGTTGCC AGCCATCTGT TGTTTGCCCC TCCCCCGTGC CTTCCCTGAC CCTGGAAGGT	2760
GCCACTCCCA CTGTCCCTTC CTAATAAAAT GAGGAAATTG CATCGCATTG TCTGAGTAGG	2820
TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA TTGGGAAGAC	2880
AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCTT CTGAGGCGGA AAGAACCAGC	2940
TGGGGCTCTA GGGGGTATCC CCACGCGCCC TGTAGCGGCG CATTAAGCGC GGCGGGTGTG	3000

GTGGTTACGC GCAGCGTGAC CGCTACACTT GCCAGCGCCC TAGCGCCCGC TCCTTTCGCT	3060
TTCTTCCCTT CCTTTCCTCGC CACGTTCTGCC GGCTTTCCCC GTCAAGCTCT AAATCGGGGC	3120
ATCCCTTTAG GGTTCGATT TAGTGCTTTA CGGCACCTCG ACCCCAAAAA ACTTGATTAG	3180
GGTGATGGTT CACGTAGTGG GCCATCGCCC TGATAGACGG TTTTTCGCCC TTTGACGTTG	3240
GAGTCCACGT TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT CAACCCTATC	3300
TCGGTCTATT CTTTTGATTT ATAAGGGATT TTGGGGATT CGGCCTATTG GTTAAAAAAT	3360
GAGCTGATTT AACAAAAATT TAACGCGAAT TAATTCTGTG GAATGTGTGT CAGTTAGGGT	3420
GTGGAAAGTC CCCAGGCTCC CCAGGCAGGC AGAAGTATGC AAAGCATGCA TCTCAATTAG	3480
TCAGCAACCA GGTGTGGAAA GTCCCCAGGC TCCCCAGCAG GCAGAAGTAT GCAAAGCATG	3540
CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC GCCCCTAACT	3600
CCGCCCAGTT CCGCCCATT CCGCCCCAT GGCTGACTAA TTTTTTTTAT TTATGCAGAG	3660
GCCGAGGCCG CCTCTGCCTC TGAGCTATT CAGAAGTAGT GAGGAGGCTT TTTTGGAGGC	3720
CTAGGCTTTT GCAAAAAGCT CCCGGGAGCT TGTATATCCA TTTTCGGATC TGATCAAGAG	3780
ACAGGATGAG GATCGTTTCG CATGATTGAA CAAGATGGAT TGCACGCAGG TTCTCCGGCC	3840
GCTTGGGTGG AGAGGCTATT CGGCTATGAC TGGGCACAAC AGACAATCGG CTGCTCTGAT	3900
GCCGCCGTGT TCCGGCTGTC AGCGCAGGGG CGCCCGGTTT TTTTGTCAA GACCGACCTG	3960
TCCGGTGCCC TGAATGAACT GCAGGACGAG GCAGCGCGGC TATCGTGGCT GGCCACGACG	4020
GGCGTTCCTT GCGCAGCTGT GCTCGACGTT GTCACTGAAG CGGGAAGGGA CTGGCTGCTA	4080
TTGGGCGAAG TGCCGGGGCA GGATCTCCTG TCATCTCACC TTGCTCCTGC CGAGAAAGTA	4140
TCCATCATGG CTGATGCAAT GCGGCGGCTG CATACTGCTT ATCCGGCTAC CTGCCCATT	4200
GACCACCAAG CGAAACATCG CATCGAGCGA GCACGTACTC GGATGGAAGC CGGTCTTGTC	4260
GATCAGGATG ATCTGGACGA AGAGCATCAG GGGCTCGCGC CAGCCGAAGT GTTCGCCAGG	4320
CTCAAGGCGC GCATGCCCGA CGGCGAGGAT CTCGTCGTGA CCCATGGCGA TGCCTGCTTG	4380
CCGAATATCA TGGTGGAAAA TGGCCGCTTT TCTGGATTCA TCGACTGTGG CCGGCTGGGT	4440
GTGGCGGACC GCTATCAGGA CATAGCGTTG GCTACCCGTG ATATTGCTGA AGAGCTTGGC	4500
GGCGAATGGG CTGACCGCTT CCTCGTGCTT TACGGTATCG CCGCTCCCGA TTCGCAGCGC	4560
ATCGCCTTCT ATCGCCTTCT TGACGAGTTC TTCTGAGCGG GACTCTGGGG TTCGAAATGA	4620
CCGACCAAGC GACGCCCAAC CTGCCATCAC GAGATTTCTG TTCCACCGCC GCCTTCTATG	4680

AAAGGTTGGG CTTCGGAATC GTTTTCCGGG ACGCCGGCTG GATGATCCTC CAGCGCGGGG	4740
ATCTCATGCT GGAGTTCTTC GCCCACCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA	4800
AATAAAGCAA TAGCATCACA AATTTACAAA ATAAAGCATT TTTTTCAC TG CATTCTAGTT	4860
GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG TATACCGTCG ACCTCTAGCT	4920
AGAGCTTGGC GTAATCATGG TCATAGCTGT TTCCTGTGTG AAATTGTTAT CCGCTCACAA	4980
TTCCACACAA CATAAGAGCC GGAAGCATAA AGTGTAAGC CTGGGGTGCC TAATGAGTGA	5040
GCTAACTCAC ATTAATTGCG TTGCGCTCAC TGCCCGCTTT CCAGTCGGGA AACCTGTCGT	5100
GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG CGGTTTGC GT ATTGGGCGCT	5160
CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCTG TCGGCTGCGG CGAGCGGTAT	5220
CAGCTCACTC AAAGGCGGTA ATACGGTTAT CCACAGAATC AGGGGATAAC GCAGGAAAGA	5280
ACATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT	5340
TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACA AAAA TCGACGCTCA AGTCAGAGGT	5400
GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC	5460
GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC CGCCTTTCTC CCTTCGGGAA	5520
GCGTGCGCT TTCTCAATGC TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTGCT	5580
CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA	5640
ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG	5700
GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC	5760
CTAACTACGG CTACACTAGA AGGACAGTAT TTGGTATCTG CGCTCTGCTG AAGCCAGTTA	5820
CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT GGTAGCGGTG	5880
GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT	5940
TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTAA GGGATTTTGG	6000
TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATECTTTT AAATTAAAAA TGAAGTTTAA	6060
AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG TTACCAATGC TTAATCAGTG	6120
AGGCACCTAT CTCAGCGATC TGTCTATTTT GTTCATCCAT AGTTGCCTGA CTCCCCGTCG	6180
TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC	6240
GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG	6300
AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT TGTTGCCGGG	6360
AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA CGTTGTTGCC ATTGCTACAG	6420

GCATCGTGGT GTCACGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT	6480
CAAGGCGAGT TACATGATCC CCCATGTTGT GCAAAAAAGC GGTAGCTCC TTCGGTCCTC	6540
CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTATCACT CATGGTTATG GCAGCACTGC	6600
ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT GAGTACTCAA	6660
CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG CTCTTGCCCC GCGTCAATAC	6720
GGGATAATAC CGCGCCACAT AGCAGAACTT TAAAAGTGCT CATCATTTGA AAACGTTCTT	6780
CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTGAGATC CAGTTCGATG TAACCCACTC	6840
GTGCACCCAA CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA	6900
CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT TGAATACTCA	6960
TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG TTATTGTCTC ATGAGCGGAT	7020
ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT TCCGCGCACA TTTCCCCGAA	7080
AAGTGCCACC TGACGTCGAC GGATCGGG	7108

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTCGAGAAAT CATAAAAAAT TTATTGCTT TGTGAGCGGA TAACAATTAT AATAGATTCA	60
ATTGTGAGCG GATAACAATT TCACACAGAA TTCATTAAAG AGGAGAAATT AACTATGAGA	120
GGATCGCATC ACCATCACCA TCACGGATCC CTGGTTCTGT TTGAAGGGGA CGAGGTGTAT	180
TCCACCATCC GGAAGCAGGA ATACAATGGG AAGATCCCTC GGTTCGCGCC CATCCGGGGC	240
GAGAGTGAGC TGTACACCAG TGATACTGTC ATGCAGAACC CACAGTTCAT CAAAGCCACC	300
ATCGTGCACC AAGACCAGGC TTACGATGAC AAGATCTACT ACTTCTTCCG AGAGGACAAT	360
CCTGACAAGA ATCCTGAGGC TCCTCTCAAT GTGTCCCGTG TGGCCCAGTT GTGCAGGGGG	420
GACCAGGGTG GGGAAAGTTC ACTGTCAGTC TCCAAGTGA AACTTTTCT GAAAGCCATG	480
CTGGTATGCA GTGATGCTGC CACCAACAAG AACTTCAACA GGCTGCAAGA CGTCTTCCTG	540

CTCCCTGACC CCAGCGGCCA GTGGAGGGAC ACCAGGGTCT ATGGTGTTTT CTCCAACCCC	600
TGGAACACT CAGCCGTCTG TGTGTATTCC CTCGGTGACA TTGACAAGGT CTTCCGTACC	660
TCCTCACTCA AGGGCTACCA CTCAAGCCTT CCAACCCGC GGCCTGGCAA GTGCCTCCCA	720
GACCAGCAGC CGATACCCAC AGAAAGCTTA ATTAGCTGAG CTTGGACTCC TGTTGATAGA	780
TCCAGTAATG ACCTCAGAAC TCCATCTGGA TTTGTTCAGA ACGCTCGGTT GCCGCCGGGC	840
GTTTTTTATT GGTGAGAATC CAAGCTAGCT TGGCGAGATT TTCAGGAGCT AAGGAAGCTA	900
AAATGGAGAA AAAAATCACT GGATATACCA CCGTTGATAT ATCCCAATGG CATCGTAAAG	960
AACATTTTGA GGCATTTTCA TCAGTTGCTC AATGTACCTA TAACCAGACC GTTCAGCTGG	1020
ATATTACGGC CTTTTTAAAG ACCGTAAAGA AAAATAAGCA CAAGTTTTAT CCGGCCTTTA	1080
TTCACATTCT TGCCCGCCTG ATGAATGCTC ATCCGGAATT TCGTATGGCA ATGAAAGACG	1140
GTGAGCTGGT GATATGGGAT AGTGTTTACC CTTGTTACAC CGTTTTCCAT GAGCAAACCTG	1200
AAACGTTTTT ATCGCTCTGG AGTGAATACC ACGACGATTT CCGGCAGTTT CTACACATAT	1260
ATTCGCAAGA TGTGGCGTGT TACGGTGAAA ACCTGGCCTA TTTCCCTAAA GGGTTTATTG	1320
AGAATATGTT TTTCGTCTCA GCCAATCCCT GGGTGAGTTT CACCAGTTTT GATTTAAACG	1380
TGGCCAATAT GGACAAC TTCGCCCCCG TTTTCACCAT GGGCAAATAT TATACGCAAG	1440
GCGACAAGGT GCTGATGCCG CTGGCGATTG AGGTTTATCA TGCCGTCTGT GATGGCTTCC	1500
ATGTCGGCAG AATGCTTAAT GAATTACAAC AGTACTGCGA TGAGTGCCAG GCGGGGGCGT	1560
AATTTTTTTT AGGCAGTTAT TGGTGCCCTT AAACGCCTGG GGTAAATGACT CTCTAGCTTG	1620
AGGCATCAAA TAAAACGAAA GGCTCAGTCG AAAGACTGGG CCTTTCGTTT TATCTGTTGT	1680
TTGTCGGTGA ACGCTCTCCT GAGTAGGACA AATCCGCCGC TCTAGAGCTG CCTCGCGCGT	1740
TTCGGTGATG ACGGTGAAAA CCTCTGACAC ATGCAGCTCC CGGAGACGGT CACAGCTTGT	1800
CTGTAAGCGG ATGCCGGGAG CAGACAAGCC CGTCAGGGCG CGTCAGCGGG TGTGCGGGG	1860
TGTCGGGGCG CAGCCATGAC CCAGTCACGT AGCGATAGCG GAGTGTATAC TGGCTTAACT	1920
ATGCGGCATC AGAGCAGATT GTACTGAGAG TGCACCATAT GCGGTGTGAA ATACCGCACA	1980
GATGCGTAAG GAGAAAATAC CGCATCAGGC GCTCTTCCGC TTCCTCGCTC ACTGACTCGC	2040
TGCGCTCGGT CTGTGCGCTG CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT	2100
TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG AGCAAAAGGC CAGCAAAAGG	2160
CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCCTGACG	2220

AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT	2280
ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCCTCTCC TGTTCGACC CTGCCGCTTA	2340
CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTCTCAA TGCTCACGCT	2400
GTAGGTATCT CAGTTCGGTG TAGGTCGTTT GCTCCAAGCT GGGCTGTGTG CACGAACCCC	2460
CCGTTTCAGCC CGACCGCTGC GCCTTATCCG GTAACATATCG TCTTGAGTCC AACCCGGTAA	2520
GACACGACTT ATCGCCACTG GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG	2580
TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG	2640
TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT	2700
GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTCGCAAG CAGCAGATTA	2760
CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC	2820
AGTGGAACGA AAATCAGCT TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA	2880
CCTAGATCCT TTTAAATTAA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA	2940
CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT	3000
TTCGTTTCATC CATAGCTGCC TGAATCCCCG TCGTGTAGAT AACTACGATA CGGGAGGGCT	3060
TACCATCTGG CCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACC GCTCCAGATT	3120
TATCAGCAAT AAACCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT	3180
CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGAAGCTAG AGTAAGTAGT TCGCCAGTTA	3240
ATAGTTTGCG CAACGTTGTT GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTTG	3300
GTATGGCTTC ATTCAGCTCC GGTTCCTAAC GATCAAGGCG AGTTACATGA TCCCCATGT	3360
TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTCAGAAGT AAGTTGGCCG	3420
CAGTGTTATC ACTCATGGTT ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG	3480
TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC	3540
GGCGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAA TACCGCGCCA CATAGCAGAA	3600
CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG AAAACTCTCA AGGATCTTAC	3660
CGCTGTTGAG ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT	3720
TTACTTTTAC CAGCGTTTCT GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAGG	3780
GAATAAGGGC GACACGGAAG TGTGAATAC TCATACTCTT CCTTTTCAA TATTATTGAA	3840
GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA	3900
AACAAATAGG GGTTCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC TAAGAAACCA	3960

TTATTATCAT GACATTAACC TATAAAAATA GCGTATCAC GAGGCCCTTT CGTCTTCAC 4019

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3999 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCGAGAAAT CATAAAAAAT TTATTTGCTT TGTGAGCGGA TAACAATTAT AATAGATTCA	60
ATTGTGAGCG GATAACAATT TCACACAGAA TTCATTAAAG AGGAGAAATT AACTATGAGA	120
GGATCGCATC ACCATCACCA TCACACGGAT CCGCATGCGA GCTCCAGTG GGAGGTGAGC	180
CAGGTGCCCC TGGACCTGTG TGAGGTCTAT GGCAGGGGCT GCCACGGTTG CCTCATGTCC	240
CGAGACCCCT ACTGCGGCTG GGACCAGGGC CGCTGCATCT CCATCTACAG CTCCGAACGG	300
TCAGTGCTGC AATCCATTAA TCCAGCCGAG CCACACAAGG AGTGTCCCAA CCCCAAACCA	360
GACAAGGCCC CACTGCAGAA GGTTTCCCTG GCCCCAACT CTCGCTACTA CCTGAGCTGC	420
CCCATGGAAT CCCGCCACGC CACCTACTCA TGGCGCCACA AGGAGAACGT GGAGCAGAGC	480
TGCGAACCTG GTCACCAGAG CCCCAACTGC ATCCTGTTCA TCGAGAACCT CACGGCGCAG	540
CAGTACGGCC ACTACTTCTG CGAGGCCAG GAGGGCTCCT ACTTCCGCGA GGCTCAGCAC	600
TGGCAGCTGC TGCCCGAGGA CGGCATCATG GCCGAGCACC TGCTGGGTCA TGCCTGTGCC	660
CTGGCTGCCT CCCTCTGGCT GGGGGTGCTG CCCCACTCA CTCTGGCTT GCTGGTCCAC	720
GTGAAGCTTA ATTAGCTGAG CTTGGACTCC TGTTGATAGA TCCAGTAATG ACCTCAGAAC	780
TCCATCTGGA TTTGTTCAGA ACGCTCGGTT GCCGCCGGG GTTTTTTATT GGTGAGAATC	840
CAAGCTAGCT TGGCGAGATT TTCAGGAGCT AAGGAAGCTA AAATGGAGAA AAAAATCACT	900
GGATATACCA CCGTTGATAT ATCCAATGG CATCGTAAAG AACATTTTGA GGCATTTCAG	960
TCAGTTGCTC AATGTACCTA TAACCAGACC GTTCAGCTGG ATATTACGGC CTTTTTAAAG	1020
ACCGTAAAGA AAAATAAGCA CAAGTTTTAT CCGGCCTTTA TTCACATTCT TGCCCGCCTG	1080
ATGAATGCTC ATCCGGAATT TCGTATGGCA ATGAAAGACG GTGAGCTGGT GATATGGGAT	1140
AGTGTTACAC CTTGTTACAC CGTTTTCCAT GAGCAAACCTG AAACGTTTTC ATCGCTCTGG	1200

AGTGAATACC ACGACGATTT CCGGCAGTTT CTACACATAT ATTCGCAAGA TGTGGCGTGT	1260
TACGGTGAAA ACCTGGCCTA TTTCCCTAAA GGGTTTATTG AGAATATGTT TTTCGTCTCA	1320
GCCAATCCCT GGGTGAGTTT CACCAGTTTT GATTTAAACG TGGCCAATAT GGACAACTTC	1380
TTGCCCCCG TTTTCACCAT GGGCAAATAT TATACGCAAG GCGACAAGGT GCTGATGCCG	1440
CTGGCGATTC AGGTTCATCA TGCCGTCTGT GATGGCTTCC ATGTCGGCAG AATGCTTAAT	1500
GAATTACAAC AGTACTGCGA TGAGTGGCAG GCGGGGGCGT AATTTTTTTA AGGCAGTTAT	1560
TGGTGCCCTT AAACGCCTGG GGTAATGACT CTCTAGCTTG AGGCATCAAA TAAAACGAAA	1620
GGCTCAGTCG AAAGACTGGG CCTTTCGTTT TATCTGTTGT TTGTCGGTGA ACGCTCTCCT	1680
GAGTAGGACA AATCCGCCGC TCTAGAGCTG CCTCGCGCGT TTCGGTGATG ACGGTGAAAA	1740
CCTCTGACAC ATGCAGCTCC CGGAGACGGT CACAGCTTGT CTGTAAGCGG ATGCCGGGAG	1800
CAGACAAGCC CGTCAGGGCG CGTCAGCGGG TGTTGGCGGG TGTCGGGGCG CAGCCATGAC	1860
CCAGTCACGT AGCGATAGCG GAGTGTATAC TGGCTTAACT ATGCGGCATC AGAGCAGATT	1920
GTAAGTGAGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATGCGTAAG GAGAAAATAC	1980
CGCATCAGGC GCTCTTCCGC TTCCTCGCTC ACTGACTCGC TGCGCTCGGT CTGTCGGCTG	2040
CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT	2100
AACGCAGGAA AGAACATGTG AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC	2160
GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCTGACG AGCATCACAA AAATCGACGC	2220
TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA	2280
AGCTCCCTCG TGCCTCTCC TGTTCCGACC CTGCCGCTTA CCGGATACCT GTCCGCCTTT	2340
CTCCCTTCGG GAAGCGTGGC GCTTTCTCAA TGCTCACGCT GTAGGTATCT CAGTTCGGTG	2400
TAGGTCGTTT GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC	2460
GCCTTATCCG GTAACATCG TCTTGAGTCC AACC CGGTAA GACACGACTT ATCGCCACTG	2520
GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC	2580
TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG	2640
CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT GATCCGGCAA ACAAACCACC	2700
GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT	2760
CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACCTACGT	2820
TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTAAATTAA	2880

AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA CTTGGTCTGA CAGTTACCAA 2940
 TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTTCATC CATAGCTGCC 3000
 TGACTCCCCG TCGTGTAGAT AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT 3060
 GCAATGATAC CGCGAGACCC ACGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA 3120
 GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT CCGCCTCCAT CCAGTCTATT 3180
 AATTGTTGCC GGGAAAGCTAG AGTAAGTAGT TCGCCAGTTA ATAGTTTGCG CAACGTTGTT 3240
 GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC 3300
 GGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCCATGT TGTGCAAAA AGCGGTTAGC 3360
 TCCTTCGGTC CTCCGATCGT TGTGAGAAGT AAGTTGGCCG CAGTGTATC ACTCATGGTT 3420
 ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT 3480
 GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC GGCGACCGAG TTGCTCTTGC 3540
 CCGGCGTCAA TACGGGATAA TACCGCGCCA CATAGCAGAA CTTTAAAAGT GCTCATCATT 3600
 GGAAAACGTT CTTGCGGGCG AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTCG 3660
 ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTTAC CAGCGTTTCT 3720
 GGGTGAGCAA AAACAGGAAG GCAAAAATGCC GCAAAAAGG GAATAAGGGC GACACGGAAA 3780
 TGTTGAATAC TCATACTCTT CCTTTTTCAA TATTATTGAA GCATTTATCA GGGTTATTGT 3840
 CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCCGCGC 3900
 ACATTTCCCC GAAAAGTGCC ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC 3960
 TATAAAAATA GCGGTATCAC GAGGCCCTTT CGTCTTCAC 3999

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8888 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAGCCGCACA CGGTGCTTTT CCACGAGCCA GGCAGCTCCT CTGTGTGGGT GGGAGGACGT 60
 GGCAAGGTCT ACCTCTTTGA CTTCCCCGAG GGCAAGAACG CATCTGTGCG CACGGTGAGC 120

CTCTCTCTTC CCCCAACACC CCCCTACCC TCTTATCTCC CCTCTGGCCC TGCCAAGGGT 180
 CCTCAGGGAA TCCGAGGGAG CTGGCTTCTC TTCCTAAACT GCCCCACCT CCGTATCCTA 240
 TAAATGGCTC CTGGGGGAGG CTCCCTAAAG GTAGTCCAGA TTGGAGTGGG GAGCTGGGGC 300
 GGTGTGGAGA AAAACAGGAG CTAATGGGCC TGGCCAGCTG GGCAGCGCTG CTGCGGAAAG 360
 CCCAGGCTGG AAGCTGGGCC CCAGAGCCCA TGCCTGGTCT TCTGAACCCT CTGGGECTCA 420
 GCTCTGGATA TGAGACCCTG TTTGACCTCA GGTAGATCAC TCACCCTCTC AGAGCCCCAG 480
 TTGCTCATCT GTCAGATGAG AATAATGGTT GCTTCCTTTG GGGCTTATCC TGAGGCTGTG 540
 TGGAAAGCAT TTCAGGGGTA CCTCACCCCT GGCAGATTGA ACTAATGCTT CTCCCCTTCC 600
 CCAGGTGAAT ATCGGCTCCA CAAAGGGGTC CTGTCTGGAT AAGCGGGTGA GCGGGGGAGG 660
 GATCTGGAGG GGTCTGAGCC ACTTGGTAAA GGGAGAGGAG ACCCTGAGGG TCTAAGGAAG 720
 GAAGCATGGC CCTGCCCCAC GAGTCCCAGA CTGATGGGGA GACGTGGTCC TCTGTGCTTA 780
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 TGGCGAGATG AGAGGCTACG CCCCTTCAG CCCGGACGAG AACTCCCTGG TTCTGTTTGA 1320
 AGGTTGGGGC ATGCTTCGGA ACTGGGCTGG GAGCAGGATG GTCAGCTCTT TGTCCAGTGT 1380
 CCGGAGGAGG GACTTCCAGG AGCTGCCTGC CCTTACTCAT TTCTCCCTCC CACTGACCCC 1440
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 GGTCCCCAGG AGCCAAAGTT TATCCTCTGC TGAGTTCACG TGGAGGCAGC CCCCCAACTC 1860

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GCAAAACAGG	TGTGGGGTGG	AGGTGCAGGG	TCTAGGGCCC	CTCGGGGAGT	TGGACCTGAT	2040
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CTCTCAATGT	GTCCCGTGTG	GCCCAGTTGT	GCAGGGTGAA	CACGGGCGTG	AGGGCTGCTG	2340
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ATGGCGTGTG	AGCGTGTGTA	TGATGGGGTG	TGTGTGTGTG	TGTGTGTGTG	TGTTTTGCCT	2580
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CCAGGGTCTA	TGGTGTTTTC	TCCAACCCCT	GGTGAGTGGC	CCTTGTCTTG	GGGCCGGGGC	3120
TGGCATTGGT	TCAGTGTCCA	GTAGGGACAG	GAGGCCCTTG	GCCCTGCTGA	GGGCCTCCCT	3180
GGTGTGGCAG	GAGCAGGGGC	TGCAGGCTCA	AGAGGCTGGG	CTGTTGCTGG	GTGTGGGGTG	3240
GGGGGACAGC	CAGTGCGATG	TATGTACTGT	TGTGTGAGTG	AGTCTGCACT	CATGGGTGTG	3300
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GGGTGCTATT	ACACCTGCTC	AGGCACTGCC	TGAGCCCCGAT	AATTCACACT	TCTTAATCAC	3480
TCTCATTGAT	TGAACACACG	GCAGGCGGAA	GTGTTGGGTG	TGTGTGGGGA	GAGTTAGGGA	3540

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GCCCAGCCCT CCTTCTGCCT CACCTCCCAC CACCCCACTG ACCTGGGCCT GCTCTCCTTG	4140
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(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

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GTGCCGCTGG CGACCTGCGT TTCACCCTGC CATAAAGAAA CTGTTACCCG TAGGTAGTCA	5580
CGCAACTCGC CGCACATCTG AACTTCAGCC TCCAGTACAG CGCGGCTGAA ATCATCATT	5640
AAGCGAGTGG CAACATGGAA ATCGCTGATT TGTGTAGTCG GTTTATGCAG CAACGAGACG	5700
TCACGGAAAA TGCCGCTCAT CCGCCACATA TCCTGATCTT CCAGATAACT GCCGTCACTC	5760
CAACGCAGCA CCATCACC GC GAGGCGGTTT TCTCCGGCGC GTAAAAATGC GCTCAGGTCA	5820
AATTCAGACG GCAAACGACT GTCCTGGCCG TAACCGACCC AGCGCCCGTT GCACCACAGA	5880
TGAAACGCCG AGTTAACGCC ATCAAAAATA ATTGCGTCTT GGCCTTCCTG TAGCCAGCTT	5940
TCATCAACAT TAAATGTGAG CGAGTAACAA CCCGTCGGAT TCTCCGTGGG AACAAACGGC	6000
GGATTGACCG TAATGGGATA GGTACGTTG GTGTAGATGG GCGCATCGTA ACCGTGCATC	6060
TGCCAGTTTG AGGGGACGAC GACAGTATCG GCCTCAGGAA GATCGCACTC CAGCCAGCTT	6120

TCCGGCACCG CTTCTGGTGC CGGAAACCAG GCAAAGCGCC ATTCGCCATT CAGGCTGCGC	6180
AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT TACGCCAGCT GGCGAAAGGG	6240
GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC ACGACGTTGT	6300
AAAACGACGG GATCTATCAT TTTTAGCAGT GATTCTAATT GCAGCTGCTC TTTGATACAA	6360
CTAATTTTAC GACGACGATG CGAGCTTTTA TTCAACCGAG CGTGCATGTT TGCAATCGTG	6420
CAAGCGTTAT CAATTTTTC A TTATCGTATT GTTGACATC AACAGGCTGG ACACCACGTT	6480
GAACTCGCCG CAGTTTTGCG GCAAGTTGGA CCCGCCGCGC ATCCAATGCA AACTTTCCGA	6540
CATTCTGTTG CCTACGAACG ATTGATTCTT TGTCCATTGA TCGAAGCGAG TGCCTTCGAC	6600
TTTTTCGTGT CCAGTGTGGC TT	6622

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCGGATCCGC CCAGGGCCAC CTAAGGAGCG G	31
------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTGAATTCAG GAGCCAGGGC ACAGGCATG	29
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